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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=10; day=20; hr=8; min=40; sec=3; ms=930;]

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Application No: 10035091 Version No: 4.0

Input Set:

Output Set:

Started: 2008-10-18 14:59:56.534
Finished: 2008-10-18 14:59:57.965
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 431 ms
Total Warnings: 11
Total Errors: 7
No. of SeqIDs Defined: 12
Actual SeqID Count: 12

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 257	Invalid sequence data feature in <221> in SEQ ID (2)
E 257	Invalid sequence data feature in <221> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)

SEQUENCE LISTING

<110> HOGREFE, HOLLY
BORNS, MICHAEL
SORGE, JOSEPH A.

<120> HIGH FIDELITY DNA POLYMERASE COMPOSITIONS
AND USES THEREFOR

<130> 10070542-01

<140> 10035091

<141> 2001-12-21

<160> 12

<170> PatentIn version 3.5

<210> 1

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
conserved domain peptide

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<221> MOD_RES

<222> (2)..(3)

<223> Any amino acid

<400> 1

Asp Xaa Xaa Ser Leu Tyr Pro

1 5

<210> 2

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
conserved domain peptide

<220>

<221> MOD_RES

<222> (2)..(4)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (7)..(7)

<223> Any amino acid

<400> 2

Lys Xaa Xaa Xaa Asn Ser Xaa Tyr Gly
1 5

<210> 3

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
conserved domain peptide

<220>

<221> MOD_RES

<222> (2)..(3)

<223> Any amino acid

<400> 3

Thr Xaa Xaa Gly Arg
1 5

<210> 4

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
conserved domain peptide

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<222> (2)..(2)

<223> Any amino acid

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Tyr Xaa Asp Thr Asp Ser
1 5

<210> 5

<211> 3

<212> PRT

<213> Artificial Sequence

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conserved domain peptide

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 <223> Any amino acid

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 Lys Xaa Tyr
 1

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 conserved domain peptide

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 <223> Any amino acid

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 Tyr Xaa Gly Gly
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 conserved domain peptide

 <400> 7
 Ser Tyr Thr Gly Gly Phe
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 <213> Artificial Sequence

 <220>
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23

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<212> PRT
<213> Thermococcus sp.

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Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
20 25 30

Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
35 40 45

Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
50 55 60

Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val
65 70 75 80

Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
85 90 95

Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
145 150 155 160

Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys
180 185 190

Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr
195 200 205

Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu
210 215 220

Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240

Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val
245 250 255

His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu
275 280 285

Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly
290 295 300

Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr
305 310 315 320

Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
325 330 335

Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365

Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr
370 375 380

Ala Gly Gly Tyr Val	Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile	
385	390	395 400
Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His		
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Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp		
420	425	430
Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe		
435	440	445
Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys		
450	455	460
Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp		
465	470	475 480
Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr		
485	490	495
Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser		
500	505	510
Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu		
515	520	525
Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu		
530	535	540
His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala		
545	550	555 560
Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu		
565	570	575
Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys		
580	585	590
Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu		
595	600	605

Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
610 615 620

Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val
625 630 635 640

Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro
645 650 655

Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp
660 665 670

Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala
675 680 685

Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu
690 695 700

Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe
705 710 715 720

Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln
725 730 735

Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys
740 745 750

Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp
755 760 765

Leu Lys Pro Lys Gly Lys Lys Lys
770 775

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<211> 2331
<212> DNA
<213> Thermococcus sp.

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ctcctcaggg acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc 180
agggtcgtta aggttaagcg cgcggagaag gtgaagaaaa agttcctcgg caggtctgtg 240

gaggtctggg tctctactt cacgcacccg caggacgttc cggcaatccg cgacaaaata	300
aggaagcacc ccgcggtcat cgacatctac gagtacgaca tacccttcgc caagcgctac	360
ctcatagaca agggcctaata cccgatggaa ggtgaggaag agcttaaact catgtccttc	420
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gttgaggttg tctccaccga gaaggagatg attaagcgct tcttgagggt cgtaaggag	600
aaggaccccg acgtgctgat aacatacaac ggcgacaact tcgacttcgc ctacctgaaa	660
aagcgctgtg agaagcttgg cgtgagcttt accctcggga gggacgggag cgagccgaag	720
atacagcgca tgggggacag gtttgcggtc gaggatgaag gcagggatca cttcgacctt	780
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gcctacgaga ggaacgaact cgctcccaac aagcccgcg agagggagct ggcgaggaga	1140
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ttctgcaagg acttccccg cttcattccg agcctgctcg gaaacctgct ggaggaaagg	1380
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ggcaagataa ccacgcgcgg gcttgagata gtcaggcgcg actggagcga gatagcgaag	1860
gagacgcagg cgagggtttt ggaggcgata ctcaggcacg gtgacgttga agaggccgtc	1920

agaattgtca gggaagtcac cgaaaagctg agcaagtacg aggttccgcc ggagaagctg 1980
gttatccacg agcagataac gcgcgagctc aaggactaca aggccaccgg cccgcacgta 2040
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tacatcgttc tgaagggtc cggaaggata ggcgacaggg cgattccctt cgacgagttc 2160
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<211> 775

<212> PRT

<213> *Pyrococcus furiosus*

<400> 12

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20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245 250 255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
290 295 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305 310 315 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
325 330 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
355 360 365

Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser

370

375

380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400

Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
420 425 430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
435 440 445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
450 455 460

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465 470 475 480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
485 490 495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
515 520 525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545 550 555 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
565 570 575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
580 585 590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
595 600 605